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OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 03:28:40 : Search time 64 seconds  
(without alignments)  
13220.644 Million cell updates/sec

Title: US-09-784-340-1

Perfect score: 2759

Sequence: 1 caaccatgcagatcagctgt.....ctgcagccgttaccgtacgc 2759

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/prodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B.COMB.seq: \*  
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4: /cgn2\_6/prodata/1/ina/5B.COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/5A.COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/5B.COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	775.6	28.1	2107	4 US-09-180-852-1	Sequence 1, Appl1
2	574	20.8	1413	4 US-09-813-918-1	Sequence 1, Appl1
3	329	11.9	2339	5 PCT-US92-00282-2	Sequence 2, Appl1
4	319.8	11.6	2336	5 PCT-US92-00282-1	Sequence 1, Appl1
5	145.6	5.3	391	4 US-09-370-838-21	Sequence 21, Appl1
6	97.4	3.5	1561	5 PCT-US82-00282-25	Sequence 25, Appl1
7	83.8	3.0	783	5 PCT-US92-00282-22	Sequence 22, Appl1
8	72.2	2.6	1008	5 PCT-US92-00282-10	Sequence 10, Appl1
9	62.4	2.3	1448	5 PCT-US92-00282-16	Sequence 16, Appl1
10	60	2.2	1066	5 PCT-US92-00282-14	Sequence 14, Appl1
11	57.6	2.1	19124	2 US-08-487-8258-13	Sequence 13, Appl1
12	55.4	2.0	1190	5 PCT-US92-00282-18	Sequence 18, Appl1
13	55	2.0	513	5 PCT-US92-00282-20	Sequence 20, Appl1
14	53.8	1.9	5852	1 US-07-867-106-2	Sequence 2, Appl1
15	52.6	1.9	1197	5 PCT-US92-00282-12	Sequence 12, Appl1
16	50.6	1.8	1800	6 5180581-1	Patent No. 5180581
17	50.6	1.8	2793	1 US-08-281-916-5	Sequence 5, Appl1
18	50.6	1.8	2793	2 US-08-460-725-7	Sequence 7, Appl1
19	50.2	1.8	665	2 US-08-883-795A-36	Sequence 36, Appl1
20	50.2	1.8	1779	4 US-09-323-427-1	Sequence 1, Appl1
21	50.2	1.8	1779	4 US-09-323-427-2	Sequence 2, Appl1
22	50.2	1.8	1779	4 US-09-812-642-1	Sequence 1, Appl1
23	50.2	1.8	1779	4 US-09-812-642-2	Sequence 2, Appl1
24	49.4	1.8	168575	4 US-07-426-290-1	Sequence 1, Appl1
25	49.4	1.8	660	1 US-07-991-867B-32	Sequence 32, Appl1
26	49.2	1.8	660	1 US-08-107-755A-32	Sequence 32, Appl1
27	49.2	1.8	660	2 US-08-544-332-32	Sequence 32, Appl1

C 28	49.2	1.8	660	4 US-09-370-861A-32	Sequence 32, Appl1
C 29	49.2	1.8	1511	1 US-07-991-867B-8	Sequence 8, Appl1
C 30	49.2	1.8	1511	1 US-08-107-755A-8	Sequence 8, Appl1
C 31	49.2	1.8	1511	2 US-08-544-332-8	Sequence 8, Appl1
C 32	49.2	1.8	1511	4 US-09-370-861A-8	Sequence 8, Appl1
C 33	49.2	1.8	4810	3 US-08-852-629-11	Sequence 11, Appl1
C 34	49.2	1.8	4838	3 US-08-852-629-15	Sequence 15, Appl1
C 35	49.2	1.8	8920	2 US-08-446-855A-1	Sequence 1, Appl1
36	49	1.8	8920	4 US-09-150-741-1	Sequence 1, Appl1
37	48.8	1.8	1669	4 US-08-522-421-1	Sequence 1, Appl1
C 38	48.6	1.8	20674	4 US-09-641-638-651	Sequence 651, App
C 39	48.4	1.8	5852	1 US-07-867-106-2	Sequence 2, Appl1
C 40	47.8	1.7	20674	4 US-09-641-638-651	Sequence 651, App
41	47.6	1.7	837	4 US-08-998-416-288	Sequence 288, App
42	47.6	1.7	1364	1 US-08-265-087-3	Sequence 3, Appl1
43	47.6	1.7	1364	1 US-08-521-493-3	Sequence 3, Appl1
44	47.6	1.7	1364	2 US-08-965-688-3	Sequence 3, Appl1
45	47.6	1.7	1364	4 US-09-260-173-3	Sequence 3, Appl1

#### ALIGNMENTS

```
RESULT 1
US-09-180-852-1
; Sequence 1, Application US/09180852
; Patent No. 6287834
; GENERAL INFORMATION:
; APPLICANT: BELANGER, Alain
; APPLICANT: HUM, Dean W.
; APPLICANT: BEAULIEU, Martin
; APPLICANT: LEVESQUE, Eric
; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
; FILE REFERENCE: DIPHOSPHO-GLUCURONOSYLTRANSFERASE
; CURRENT APPLICATION NUMBER: US/09/180,852
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00338
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1644)
US-09-180-852-1
Query Match      28.1%; Score 775.6; DB 4; Length 2107;
Best Local Similarity 68.3%; Pred. No. 2.7e-174;
Matches 1110; Conservative 0; Mismatches 504; Indels 12; Gaps 2;
QY 35 ATATAGAGTCTGACAAAGTCAGCTTGTGTAATTCCTGCTCGACGCTCTTCTGT--GTT 91
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 46 ACCAGGATGCTCTGAAATGATGATGCTGCTCTGCTGATGACGAGCTCAGATTGTACTT 105
QY 92 GCGTGTGATTCGTGGGAAGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 151
DB 106 AGCTCTGGAGTGTGTGAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 165
QY 152 GTCAAGTCATTCCTAGAGAGCTCATAGTAGAGAGCCATGAGTAAACATGATGACTCAC 211
DB 166 ATGAAGCATCTCTGAGAGAGCTTGTTCACAGAGGCTCATGAGGATGTGTGTGACTCT 225
QY 212 TCAAGCTTCCTGTAATTCATGACAGAGAGCTTGTGATGAAATTTGAGTGTGCTCAT 271
DB 226 TCGGCTTCTTCTTCTGCAATGCAAGTAATTCATCTGTAATTAATTAAGTAAATTCCT 285
QY 272 ATGCACAGACAGACAGACAGAAATGAATATTT-----GTTGACCTAGCTCTG 322
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286 ACATCTTTAACTAAATATGATTTGGAGATTTTATGAAATGTTCGATACATGACACA 345
QY 323 AATGCTTGGCAGGCTTATCAACCTGGCAATCAGTTATATAATTAATGATTTTGT 382
Db 346 TATAGTATTTCAAAAAATACATTTTGTGTCATATTTTTCACAAATACAAAGATTTGTGG 405
QY 383 GAATTAAGAGAACTTTAAAAATGATGTGAGAGCTTTTATCTCAATTCAGAGCCTTATG 442
Db 406 GAATATTTCTACATATTAATATAAAAGCTGTGAAGATGACAGTTTGAACAAGAACTTATG 465
QY 443 AAGAAGCTAGAGAAACCACTACAGATGATATGCTTATAGACCTGATACCTGTGGA 502
Db 466 AGAATACTACAAAGGTAAATTTGATGTCTTCCTGCGAGATGCGGTAAATCCGTGGGT 525
QY 503 GACCTGATGCTGATGCTTGTGACGTCCCTTTGTGCTCACACTTAGAATTTCTGTAAGA 562
Db 526 GAGCTGCTGGCTGAACATTAACATACCCCTTCTGACAGTCTCCGCTTCTGTGTGGC 585
QY 563 GGCATATGAGCAAGCACTGTGGGAACCTCCACCTCCACTTCTGTATGCTACCTGGCT 622
Db 586 TACACAGTTGAGAAAGATGAGGAGATTTCTGTTCCCTCTCTATGATACCTGTGTT 645
QY 623 ATGACAGACTAACAGACAGATGACCTTTCTGGAAGAGTAATAAATTCATGCTTTCA 682
Db 646 ATGTCAGATTTAATGATCAATGATTTTTCATGAGAGATATAAATAATGATATATAG 705
QY 683 GTTTTGTCCACTTCTGAGATTCAGATTTAGCATATCTTTTGGGAGAGCTTTTATAGT 742
Db 706 CTATATTTTGTCTTTGTGTTTCAAGCATATGATGTAAGAAAGTGACCACTTTTATAGT 765
QY 743 AAGCATTTAGGAAGGCCACTACATTTATGAGAGCTGTGGAAAAAGCTGAGATTTGGCTA 802
Db 766 GAACTTCTAGAAACACCACTACATTTATTTAGCAATGGGGAAGAGCTGAATGTGGCTC 825
QY 803 ATACAAATATTTGGATTTTGAATTTCCCTCAACATACCAACTTACCTTGAATTTGT 862
Db 826 ATTCGAACCTTATGAGATTTTGAATTTCCCTGCGCATCTTACCAAAATGTTGATTTGT 885
QY 863 GGAGGATTTGCCTGTAACCTGCCAAGCTTTGCTTAAGAAATGGAATTTTGTCCAG 922
Db 886 GGAGGACTTCACTGTAAACCAAGCAACCTTGTGCTTAAGAAATGGAAGATTTGTGAG 945
QY 923 AGTTCAGGGAAGATGATTTGTGTTTCTCTGGGGTACTGTTCCTCAAAATGTTACA 982
Db 946 AGCTCTGAGAAATGATTTGTGTGTTTCTCTGGGGTGTGATGATAGTAACATGTCA 1005
QY 983 GAAGAAAGGCTAATATATCTGCTTCAAGCCTTGGCCAGATCCCAAGAGGTGTATAG 1042
Db 1006 GAAGAAAGTGCACATGATTTGACATGACCCCTTGGCCAGATCCCAAGAGGTGTATAG 1065
QY 1043 AGGTACAAAGAAAAAACCATCCATTTAGAGCCATCTCGGCTGTATGATGTGATA 1102
Db 1066 AGATTGTATGCAAGAAACCAAAATACCTTGTAGTTCATCTGCACTGTATATAAGGTGA 1125
QY 1103 CCCAGATGATCTTCTGTCATCCCAAAACCAAGCTTTTATCAGCATGTTGGAATG 1162
Db 1126 CCCAGATGATCTTCTGTCATCCCAAAACCAAGCTTTTATACATGATGTGGAATG 1185
QY 1163 AATGGATCTATGAAGCTATTTACCATGGGCTCCTATGTGGGATTTCCATATTTGCT 1222
Db 1186 AATGGATCTATGAAGCTATTTACCATGGGATCCTATGTGGGATTTCCATATTTGCTG 1245
QY 1223 GATCAGCTTGTATACATAGCTTCACATGAAGCCAAAGAGAGCTGTGAAATTAACCTTC 1282
Db 1246 GATCAGCTTGTATACATAGCTTCACATGAAGCCAAAGAGAGCTGTGAAATTAACCTTC 1305
QY 1283 AAAATATGAGAAGGAGATTTACTGAGGGCTTGAAGACGATTAACGATTCGCT 1342
Db 1306 AGGACCATGTCAAGTATGATTTGCTCAATGATTAAGTCAATTAATGATACCTTATC 1365
QY 1343 TATTAAGAAATGCTATGATTTATCAAGAAATTCACATGATCAACCTGTAAGCCCTTA 1402

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Db 1366 TATTAAGAAATATCATGAATATATCAAGAATTCATCATGATCAACCGGTGAAGCCCTG 1425
QY 1403 GATCAGACATGCTTCTGATCGATGATTTGTGATGGCCCAAGAGAGCAACCTGCGA 1462
Db 1426 GATCAGACATGCTTCTGATCGATGATTTGTGATGGCCCAAGAGAGCAACCTGCGG 1485
QY 1463 TCAGCTCCCATGACCTCACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1522
Db 1486 GTGCGACGCCCAACCTCACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1545
QY 1523 CTGACCTGTGTGCACTGATATATCTTGTTCACAAAATGTTTTTATTTCTGTCAA 1582
Db 1546 CTGCGCTGCGGCACTATGATATTTATGATTCACAAAATGTTTTTCTGTTTCTCGGA 1605
QY 1583 AAATTAATAAATACTAGAAGATGAAAGAGGAGATATGATCTTCCAAATTCAGAAGA 1642
Db 1606 AAGCTTGCCAAACAGAGAAAGAGAGAAAGAGATTAATGATATCAAAAGCTGAAAGT 1665
QY 1643 ACCTGA 1648
Db 1666 GATGCA 1671

RESULT 2
US-09-813-918-1
: Sequence 1, Application US/09813918
: Patient No. 6383789
: GENERAL INFORMATION:
: APPLICANT: WEBSTER, Marion et al.
: TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
: TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
: TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: C1001175
: CURRENT APPLICATION NUMBER: US/09/813,918
: CURRENT FILING DATE: 2001-03-22
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1413
: TYPE: DNA
: ORGANISM: Human
US-09-813-918-1

Query Match 20.8%; Score 574; DB 4; Length 1413;
Best Local Similarity 78.4%; Pred. No. 1,1e-126;
Matches 688; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 754 AAGGCCACTACATTTATGTGAGACTGTGGGAAAGCTGAGATGCTTAATACGAACATA 813
Db 520 ACGACCCACTACCTTATTTGAGACAAATGGAAGAACTGACATATGCTTATGCGAAACCC 579
QY 814 TTGGATTTTGAATTTCTCAACCATTACCACCTTAATTTAGTTGTGAGAGATTGCA 873
Db 580 CTGAGATTTCAATTTCTCATCACTTCTTACCAACCTGTGATTTGTTGGAGATTCCA 639
QY 874 CTGTAACCTGCAAAAGCTTTGCTTAAGAAATGGAATTTTGTCCAGAGTTCCAGGGA 933
Db 640 CTGCAAACTGCAAAACCCCTACCTAAGAAATGAGAGAGTTGTACAGAGCTCGAGGA 699
QY 934 AGATGTAATGTGTGTTTCTGTGGGCTCACTGTTCAAAATGTTTACAGAAAGAAAGCC 993
Db 700 AAATGTTGTGTGTTGTTTCTGTGGGCTCAAGTATGATGATGATGATGATGATGATGATG 759
QY 994 TAATATCATGCTTATGAGCTTTGCCCAATCCCAAGAAAGGTATGATGAGAGTACAAAG 1053
Db 760 CAATTAATTTGCAAGCCCTTGGCCAGATCCCAAAAGGTTCTGTGAGATTTGACGG 819
QY 1054 AAAAAACCATCAATTAAGGAGCAATATCGGCTGATGATGATGATGATGATGATGATGATG 1113
Db 820 GAATTAACCAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 879
QY 1114 TCTTCTGTGATCCCAAAACCAAGCTTTTATCACTCATGTGTGAATGATGATGATGATGAT 1173

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Db	880	CTTCTTAGGTCATCCAAAACGAGACCTTTTATTA	CTCTGATGGAGCCATGGCATGTGTA	1233
QY	1174	TGAAGCTATTATTAACCATGGGGTCCCTATG	TGGGAGTTCCCATATTGGTGATCACTTGA	1233
Db	940	TGAGGCAATCTACCATTGGATGGATCCCATGG	TGGGCATCCATTGTTTTGATCAACCTGA	999
QY	1234	TAACTATGCTCACTGAAGGCCAAAGGAGCAG	CTGTAGAAATTAACCTTCAAAATGATGAC	1293
Db	1000	TAACTATGCTCACTGAAGGCCAAAGGAGCAG	CTGTATGATTTGACCTTCACACATGTC	1059
QY	1294	AAGGAGATTTACTGAGGGCTTTGGAAGCAG	TCATTAACGATTCCTCTTAATAAGAA	1353
Db	1060	GAGTACAGACCTGCTGATATCACTGGAAGCA	GATTAATTAATGATCCTTTATATTAAGAGAA	1119
QY	1354	TGCTATGAGATTTATCAAGAAATTCACCAT	GATCAACCTGTAAAGCCCTAGATGAGCAGT	1413
Db	1120	TATTATGAATTTATCAAGATTTCAATCATG	ATCAACCATTAAGGCCCTGGATCGAGCAGT	1179
QY	1414	CTTCTGATGAGATTTGTCATGGCCCAAAAGG	AGCCAAAGCAGCCTGCGATCACTGCCCA	1473
Db	1180	CTTCTGATTTGAATTTGTCTATGGCCCAAA	AGGAGCCAAACCTTTCAGATGGCAGGCCA	1239
QY	1474	TGACCTCACTGGTGTCCAGAGCATCTCTA	GTATGATGGTGTCTGCTGACCTGTGT	1533
Db	1240	TGACCTCACTGGTGTCCAGATCAACCACT	TTTGGATGTGATTTGGGCTTTTGCTGGCC	1299
QY	1534	GGCACTGCTATATCTTGTTCACAAATG	TTTTTATTTTCTGTCAAAAATTAATTA	1593
Db	1300	GGCACTGCTATATTTATTCATCAAAAG	TTTTGTCTGTTTCTGTGGAAGTTTGGTAG	1359
QY	1594	AACATGAAGATGAAGAAAGGGAATAGAT	CTTTCCAA	1631
Db	1360	AAAAGGAGAGGAGAAAGAGATATGATG	TCGGA	1397

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1 RESULT 3
2 PCT-US92-00282-2
3 ; Sequence 2, Application PC/TUS9200282
4 ; GENERAL INFORMATION:
5 ; APPLICANT: OMENS, IDA S.
6 ; APPLICANT: RITTER, JOSEPH K.
7 ; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
8 ; TITLE OF INVENTION: THEREIN.
9 ; NUMBER OF SEQUENCES: 40
10 ; CORRESPONDENCE ADDRESSES:
11 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
12 ; STREET: 1615 L STREET, N.W.
13 ; CITY: WASHINGTON
14 ; STATE: D.C.
15 ; COUNTRY: U.S.A.
16 ; ZIP: 20036-5601
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: PCT/US92/00282
24 ; FILING DATE: 19920110
25 ; CLASSIFICATION: 435
26 ; ATTORNEY/AGENT INFORMATION:
27 ; NAME: SCOTT, WATSON T.
28 ; REGISTRATION NUMBER: 26581
29 ; REFERENCE/DOCKET NUMBER: 91532-PCT
30 ; TELECOMMUNICATION INFORMATION:
31 ; TELEPHONE: 202-861-3000
32 ; TELEFAX: 202-822-0944
33 ; TELEX: 6714627 CUSH
34 ; INFORMATION FOR SEQ ID NO: 2:
35 ; SEQUENCE CHARACTERISTICS:
36 ; LENGTH: 2339 base pairs
37 ; TYPE: NUCLEIC ACID

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
PCT-US92-00282-2

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Query Match	11.98;	Score 329;	DB 5;	Length 2339;
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Best Local Similarity 52.5%; Pred. No. 1.2e-68;  
Matches 797; Conservation 0; Mismatches 710

Matches 797; Conservative 0; Mismatches 710; Indels 12; Gaps 3;

QY	68	CTGCTCCGAGAGCTCTCTGTGGTGGCTGGATCTGCTGGGAAAATCTCGGTGGGCC	127
Db	46	CTGCTGCTCTCTCTCACTGTCCAGCCCTGGGCTGAGAGTGGAAAAGTGTGGGGTCCC	105
QY	128	TGTGACATGAGCCATTTGGCTTAATGTCAAGGTCATTCTTAAGAGGCTCATGTAGAGGC	187
Db	106	ACTGATGGACAGCCCTGTGCTCACATGCGGGAGCGCTTGCGGGAGGCTCCATGCCAAGGC	165
QY	188	CATGAGTAAACGATATTGACTCACTCAAAAGCTTGGTTAATTGACTACAGAAAGCTTCT	247
Db	166	CACCAAGCGGTGGTCCACACCCAGAGGTGAATATGCATCAAAAGAAATTTTTC	225
QY	248	GCATTTGAAATTTGAGGTGGTCCATATGCCACAGACAGACAGAAACAGAAATGAATATT	307
Db	226	ACCTGTACAGGCTATATGCTGTTCATGAGCCCAAA-----GGAATTTGATGGCGTTACG	279
QY	308	GTTACACCTAGCTGTGAATGTCTTGCCAGGCTTTTCACCTGGCAATCAGTTATTAATTA	367
Db	280	CTGGGCTACACTCAAGGTTCTTTGAAACAGAACATCTTCTGAAGATATTCTGAAAGT	339
QY	368	AATGATTTTTTTTGTGAATTAAGAGAACTTTAAAAATGATGTGAGAGCTTTATATAC	427
Db	340	ATGCAATTTATGAACATGATTTCTTTGGCCCTTCATAGTGTGTGTGGAGCTACTGCAT	399
QY	428	AATAGAGGCTTATGAGAGAGCTACAGAAACCAACTACGATGTATATGTTATACCT	487
Db	400	AATAGGCGCCGTGATCACACCCCTGAATGTACTCTCTTGTATGTGGTTTAAACACCCC	459
QY	488	GTCATTCCTCTGTGGAGACCTGATGGCTGATGTTCTTGACATCCCTTTGTGCTACACT	547
Db	460	GTTAACTCTGTGCGGGGGGTGTGCTAGTAACTGTTCATTTCTCTCTGTGTT---TTTT	516
QY	548	AGAAATTTCTGTAGAGGCAATATGAGCGAAGCTGTGGAAACTTCCAGCTCCACTTTC	607
Db	517	TGGAGTACATTTCCATGTGACTTAGACTTTAAGGACACAGCTGTCCAAATCCTTCTCC	576
QY	608	TATGTACCTGTGCTATGACAGAGACTACACAGACAGATACCTTTCTGGAAGAGTAAAA	667
Db	577	TATTTTCTTAAGTTACTTAAGACCAATTTACAGACATACATACATTTCTGTGAAAGGCTCAAG	636
QY	668	AATTCATGCTTCAGTTTGTTCACCTCTGTGATTCAGGATTTACGATCATATTTTGG	727
Db	637	AAC---ATGCTTACCTCTGTGCGCTGTGCTTACATTTTGGCAATCTTTTCTGCCCTTAT	693
QY	728	GAAAGATTTATAGTAAGCATTTAGGAGGCCCATACATTAATGTGAGACTGTGGAAAA	787
Db	694	GCAAGTCTTGCTGTGAGCTTTTTCAGAGAGAGGTGTCAAGTGTGATGTTGTCAAGTAT	753
QY	788	GCTAGATATGCTAATACGACATATTTGGGATTTTGAATTTCTTCACCAATACCACT	847
Db	754	GCATCCCTGTGGCTGTTCACGAGGGGACTTTGTGATGTACCTCCAGCGCGATCTATGCC	813
QY	848	AACTTTATAGTTGTGGAGATTTGACTGTAAACCTGCCAAAGCTTTGGCTTAAGGAATG	907
Db	814	AACATGTCTTCAATTTGGGGCATCAACTGTGCCAACGGAGAGCCACTATCTAGGAATTT	873
QY	908	GAAATTTTGTCCAGAGTTTGAGGGGAAAGTGTATTGTGTGTGTTTCTTCTGGGCTACGT	967
Db	874	GAACTTACATTTAATGCTTCTGGAGAACATGGAATGTGTTTCTTCTTTGGGATCAATG	933
QY	968	TTTCAAAATGTTCAGAGAAAAGCTAATATCATTTGCTTTCACGCCCTTGGCCAGATCCCA	1027
Db	934	GTCACAAAAATTCACAGAGAAAGCTATAGGCAATTTGCTGATGCTTTTGGGCAAAATCCCT	993

Query Match	Best Local Similarity	Score	DB	Length
Matches 777; Conservative	52.5%; Pred. No. 1.8e-66;	0;	Mismatches 692;	Gaps 12;
TELEX: 071462/ Cosh INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2336 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA PCT-US92-00282-1				
106	TGGAAAGTCCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGATCATCTT	165		
81	TGGGAAGATACGTGGTGAATCCAGTGGATGGCAGCCACCTGGCTGACCATGCTTGGGGCCAT	140		
166	AGAAAGAGCATAGTGAAGAGGCCATGAGTAAACAGTATTGACTCACTCAAAAGCCTTTCCT	225		
141	CCAGCAGCTGCAGCAGAGAGGGGACATGAATTAATGTTCCTAGCAGCCTGAGCCCTGTTGA	200		
226	AATTGACTACAGAAAGCCTTGCATGTAATTTGGAGTGGTCCATATACAGACAGAC	285		
201	CATCAGAGCAGGAGCATTTTACACCTTGA-----AGAGTACCTGTGCCATTCACAAG	254		
286	AACAGAGAAATGAATATTTTGTGACCTAGCTGTAATGTCTTCCAGGCTTATCAAC	345		
255	GGAGATGTGAAGAGCTCTTTGTAGTCTCGGGCATATGTTTGTGAAATGATTTCTTT	314		
346	CTGGCAATCAGTTATTAATTAATGATTTTGTGTAATTAAGAGAACTTAAAT	405		
315	CCGTGACGCGTGTATCAAAACATCAAGAAATTAAGAAAGAGCTCTGTATGCTTTTGC	374		
406	GATGTGAGAGCTTATATCATCAATCAGAGCTTATGAAGAGCTACAGAAACCACTA	465		
375	TGGCTGTCCACTTACTGTGCAAAAGAGCTCATAGGCTCCCTGGCAGAAAGACGCTT	434		
466	CGATGTAATGCTTATAGACCTCTGTGATTCCTGTGAGAGACCTAGTGGTGTGC	525		
435	TGATGTATCTGACGAGCCCTTCTCTTCTTGTGAGGCCCATGTGGCCAGTACCTGTC	494		
526	AGTCCCTTTTGTGTCACACTTGAATTTCTGTAAGAGCAATATGAGAGCGAAGCTGTGG	585		
495	TCTGCCACACTGTATTC---TTCCTGATGTGACATGCCATGAGCCTGGAATTTGAGGCTAC	551		
586	GAAATCTCAGACCTCACTTCTCATGTACCTGTGCTCATGACAGACTAACAAGACAGAT	645		
552	CCAGTGGCCCCAACCACTATCTCTGAGGCCAGGCGCTCTCTCTCATATTCAGATCAT	611		
646	GACCTTCTGGAAGAGTAAATTAATCAATGCTTCAAGTTTGTTCACCTTCTGGATTC	705		
612	GACCTCTCTGAGCGGGGTGAAGAA---CATGCTCATTTGCCCTTTCACAGAACTTCTGTG	668		
706	GGATTACACATATATTTTGGGAAGACTTTTATATAGACCATTTAGAGAGCCCATAC	765		
669	CGAGCTGTTATTTCCCGTATGAGAACCTTGCCTCAGAAATTCCTTCAGAGAGGTGAC	728		
766	ATTATGTAGACTGTGGGAAGAGCAGATATGCTTATAGCAATATTTGGGATTTTGA	825		
729	TGTCAGAGACCTATTGACCTGTGATCTGTCTGTGCTGTTTGAAGTACTTTTGAAGGA	788		
826	ATTCTCAACCATACCAACCTTACCTTGTAGTTTGGAGAGTTGACCTGTAACCTGC	885		
769	TTACCTTAGGCCATCAGCCCAATATGTTTGTGTGGTAATCAACATGCTTCACCA	848		
886	CAAGACTTGGCTTAAGGAATGGAATTTTGTCCAGAGTTGAGGAGAAATGATTTGT	945		
849	AATATCCACTATCCACGGAATTTGAAGCTCAATATATGCTTTGAGAGAACTGGAATGT	908		
946	GGTGTCTTCTGGGGTCACTGTTCAAAATTTACAGAGAAAGGCTATATATCATTC	1005		
909	GGTTTCTCTTGGATCATATGCTGCAGAAATTCAGAGAAAGGCTATGGAATTC	968		





```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; PCT-US92-00282-16

Query Match
Best Local Similarity 48.5%; Score 62.4; DB 5; Length 1448;
Matches 233; Conservative 0; Mismatches 241; Indels 6; Gaps 2;

QY 451 ATGGCAATTATGAAACATATGTTCTTATCATCATATAGAGCTTGTGGAGCTACTGACAT 510
QY 428 AATCAGACGCTTATGAAGAAGCTACAGAAACCACTACGATATATGCTTATAGACCT 487
DB 511 AATGAGGCCCTGATGAGGACCTGACATGCTACTCTCTTGTATGATGATTAACAGACCCC 570
QY 488 GNGATTCCTGTGAGAGACCTGATGCTGATGCTTGCAGTCCCTTGTGTCACACTT 547
DB 571 TTTCACCTCTGGCGCGGCGGTGCTGCTAGTACCTGTGCTGCTGCTGCTGCTGCTG 630
QY 548 AGAATTTCTGTAGAGGACCAATATGAGCGAAGCTGTGGAACTTCACAGCTTCC 607
DB 631 AGGAAATTCATCATGTG---ATTAGACTTTAAGGGCACACAGTGTCCAAACCTTCCTCC 687
QY 608 TATGTACCTGTGCTTGTGAGAGACCTACAGACAGATGACCTTCTGGAAGAAAGTAAA 667
DB 688 TATATTCCTAGATTAATTAACAGACCAATTCAGACCATGATCTGTGCAAAAGGTCAG 747
QY 668 AATTCATGCTTTCAGATTTTGTTCACATCTGTGATTCAGATTAACGATATCATTTTGG 727
DB 748 AA---CATGCTACCCCTCTGCGCCCTGCTGCTACCTTTGCCATGCTGTTCTGCTCTTAT 804
QY 728 GAAGAGTTTAAATAGTAAAGCATTAAGAGGCCCACTACATTAATGAGAGCTGTGGAAAA 787
DB 805 GCAAGCCTTGCTCTGAGCTTTTTCAGAGAGAGGTGTCAGTGTGATCTTTCACGCCAT 864
QY 788 GCGAGATATGCTATAGACACATATTTGGGATTTTGAATTTCTTCAACCATCAACCT 847
DB 865 GCATCTCTGTGCTGCTTCCGAGGGAGTGTGTGATGATGATTAACCCAGGCCGATCATGCCC 924
QY 848 AACTTGAATTTGTGAGAGATTCAGCTGTAAACCTGCCAAAGCTTGGCTAAG 902
DB 925 AACATGCTCTTCATTGGGGCATCAACATGTCACAGGAGGACCTACTATCTCAGG 979

```

# RESULT 9 PCT-US92-00282-16

```

; Sequence 16, Application PC/TUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; TITLE OF INVENTION: THEREIN.
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1448 base pairs
; TYPE: NUCLEIC ACID

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; PCT-US92-00282-16

Query Match
Best Local Similarity 48.5%; Score 62.4; DB 5; Length 1448;
Matches 233; Conservative 0; Mismatches 241; Indels 6; Gaps 2;

QY 398 TTAATAATGATGTGAGAGCTTTATCTACAACTACAGACGCTTATGAAGAAGCTACAGAA 457
DB 475 TTTCATATAGCTTGTGTGAGGCTACTGCAATATGAGAGCCCTGATGAGCAACGATGCT 534
QY 458 ACCAATAGATGATATGCTTATAGACCTGTGATTTCCCTGTGAGACCTGATGCTGAG 517
DB 535 ACTTCTCTGATGTGCTTTTAATAGACCAATTTACCTGTGAGGCGACGTGCTGCTGAG 594
QY 518 TTGCTTGACGTCCTTTTGTGCTACACTTGAATTTCTGTAGAGGACCAATATGAGCA 577
DB 595 TACCTATCATTCCTCTGCTGCTGCTTTTGTGAGAGACATTCATGTC---ATTAGACTTT 651
QY 578 AGCTGTGGAAACTTCCAGCTCCACTTTCCTATGACCTGTGCTATGACAGGACTACAA 637
DB 652 AAGGCAACAGATGTCCAATTCCTTCCTATATTCCTAAGTTACTAGCAACCAATTC 711
QY 638 GACAGATACCTTTTGTGAAAGAGTAAATAATTCATGCTTTCAGTTTGTCCACTTC 697
DB 712 GACCAATGACATCTCTGCAAAAGGTCAGAA---CATGCTACCTCTGCGCCCTGCTC 768
QY 698 TGGATCAGATTAACATCATTTTGTGGAAGATTTTATAGTAGGACTTAGGAAG 757
DB 769 TACCTTGCCATGCTCTTCTGCTCTTATGCAAGCTTGCCTGAGGCTTTTTCAGAG 828
QY 758 CCCACTACATTAATGAGAGCTGTGGAAGAAGCTGATATGCTATATACCAATATTTGG 817
DB 829 GAGGTGCTAGTGTGATGATTTCTCAGCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 888
QY 818 GATTTGAATTTCTCACAACATACCACTTAACCTTGAATTTGTGAGAGATTCAGCTGT 877
DB 889 GGTATGATTAACCCAGGCGCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948

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# RESULT 10 PCT-US92-00282-14

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; Sequence 14, Application PC/TUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; TITLE OF INVENTION: THEREIN.
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 TELEX: 6714627 CUSH  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1066 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 PCT: US92-00282-14

Query Match 2.2%; Score 60; DB 5; Length 1066;  
 Best Local Similarity 44.9%; Pred. No. 3.9e-05;

Matches 360; Conservative 0; Mismatches 430; Indels 12; Gaps 3;

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OY 68 CTGCTCCGACGCTCTTCTGTTGGCTGTGAGATTCTGTGGAAAGTCGCTGTGCCCC 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 CTGCTGCTTCCTCCAGTGTCCAGCCCTGGGCTGAGAGTGAAAGTGTGTGCTGCC 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 128 TGTGACATGACCAATGCTTAATGTCAGAGTCATTCAGAGCTCATAGTGAGAGGC 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 ATTATGCGACCACTGCTGCTGAGCATGGGAGGCTTGGCGAGCTCATGCCAGAGGC 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 188 CATGAGGTACAGATTGACTCACTCAAGCCTTCGTTAATTGACTACAGAGACCTTCT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 CACGAGGAGGTCCTCCACCCAGAGGTGAATGACATCAAGAAGAACCTTTTTC 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 248 GCATTGAATTTGAGGTGCTCATATGCGACAGACAGACAGAAAGAAATGAATATTT 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 ACCCTGACACCTATGCACTTTCGCGACCCAGATGATTTGATCGCCAG-----TG 409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 308 GTTGACCTGCTGAATGCTTGTCCAGGCTTATACCTGGCAATCGATTATAAATTA 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 CTGGCCACACCACTGCTTACTTTGAAACAGAACATTTTTCGAAACAAATTTTTCGAAGT 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 368 AATGATTTTGTGTAATAGAGAACTTAAATGATGTGTGAGAGCTTTATCTAC 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 ATGGCAATGTTGAACAATATGCTTTGGCTATCATAGTCTTGTGTGAGTACTACAT 529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 428 AATCAGACGCTTATGAGAAAGCTACAGAAACCAACATGATGTAATGCTTATAGACCT 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 AATGAGGCCCTATGAGGACCTGATGCTACTTCTTGTATGTGTTTAAACAGACCC 589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 488 GTGATTCCTGTGAGAGACCTGATGCTGAGTGTGCTGCACTGCCCTTTGTGCTACACTT 547
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 GTTAACTCTGCGCGCACTGCTGCTAGTACCTGTGATTCGATTCGCTGTGTTTTTG 649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 548 AGAATTTCTGTAGAGGCAATATGAGCGAAGCTGTGGAAACTTCCAGCTCCACTTTC 607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 650 AGGACATTCATGTC---ATTAGACTTTAAGGCGACACAGTGTCCAAACCTTCCTCC 706
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 608 TATGTACCTGTGCTATGACAGAGCTACAGACAGATGACCTTTCTGAAAGATGAAA 667
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 707 TATATTCCTAGATTACTTACAAACCAATTCAGACCATGATTCATTCGAAAGGCTCAAG 766
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 668 AATTCATGCTTTCAGTTTGTTCCTGCTCTGTGATTCAGATTCAGACTATCATTTTGG 727
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 767 AAC--ATGCTCTACCTCTGGCCCTGTCTCATATTCGATTCGCTTCTGCTCTTAT 823
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 728 GAAGAGTTTATAGTAGGCAATTAGAGAGGCCCACTACATTATAGTGAAGTGTGGAAAA 787
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 824 GCCAGCCTTCCCTGAGCTTTTTCAGAGAGAGTGTGATGTGATATTTCTCACTCAT 883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 788 GCTGAGATATGCTAATACAGACATATTTGGGATTTTGAATTTCTCAACCATACCACT 847
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 884 GCATCTGTGTGCTGTTCCAGAGGGAATTTGTATGAGTACCCAGGCCAATCATGCTCC 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 848 AACTTGAAGTTTGTGAGAGAT 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 AACATGCTTTCATTTGGGCGAT 965
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```

## RESULT 11

US-08-487-826B-13  
 ; Sequence 13, Application US/08487826B

; Patent No. 5993827

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chituls, Chetan

; APPLICANT: Miller, Louis H.

; APPLICANT: Peterson, David S.

; APPLICANT: Su, Xin-zhaun

; APPLICANT: Wellens, Thomas E.

; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knodde Martens Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: California

; COUNTRY: US

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,826B

; FILING DATE: 10-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Israel, Ned

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: NIH121.001CPI

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19124 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-487-826B-13

Query Match 2.1%; Score 57.6; DB 2; Length 19124;

Best Local Similarity 45.3%; Pred. No. 0.00041;  
 Matches 150; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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OY 2271 ATTATGTCCTCAATATATTAAGAAAGAACTGAATTTCTTTCATAGAGAAATGTCATA 2330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15688 AATATATATCATTAATAACAAAAAAGAAAAAATATATTAATAATATATATTC 15747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2331 AGATATTCAGCTTAACAGATTTATTTGAGATTAAGTAAACCATTTAGAAATATGTGAT 2390
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15748 ATAAATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2391 ATTTCGATTTTATTAATTTTATTTGATGATGACCTGATTTAAATGCTATTCCTTAA 2450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15808 ATTTATTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15867
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2451 AATGATGATGATCTCAATATTTCTTATCTATTAATCAAAAGATATTAATTTAGTGA 2510
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15868 AATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15927
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2511 TAAAGAGATGCTGTTCTGGAAGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2570
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15928 TAAAAAATAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15987
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OY 2571 CGTA 2574
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Db 848 TTCCTGCAAGGGTCAGAAC---ATGCTCTACCCCTGCCCCCTGCTACATTGCCAT 904  
Qy 710 TACGACTATCATTTTGGAGAAGTTTATAGTAGGCATTAGAGGCCCTACATT 769  
Db 905 ACTTTTCTGCCCCCTTATGCAAGTCTTGCCCTCTGAGCTTTTCAGAGAGAGGTGTCAGTG 964  
Qy 770 TGTGAGACTGTGGGAAAGCTGAGATATGCTAATACGAACATATGGGATTTGAATT 829  
Db 965 GTGGATCTTGTCAGCTATGCATCCGTGTGGCTGTCCGAGGGGACTTTGTGATGACTAC 1024  
Qy 830 CCTCAACCATACCACTTACTTTGAGTTGTTGGAGATTGCACCTGTAACCTGCGCAA 889  
Db 1025 CCCAGGCCGATCATGCCCAACATGCTCTCATTTGGGGGCATCATCTGTGCCAACGGGAAG 1084  
Qy 890 GCTTGCCCTAAGG 902  
Db 1085 CCACTATCTCAGG 1097

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Job time : 143 secs

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